

SEQUENCE LISTING

<110> Tarczynski, Mitchell C
Li, Changjiang

<120> Methods and Compositions for Modifying Oil and Protein
Content in Plants

<130> 5718-113 (35718/236392)

<140>

<141>

<150> 60/226,142

<151> 2000-08-18

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 2245

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (138)..(1844)

<400> 1

cgaaaaccct cgcggcgagg agcgcctctcc gtccacaca cgcgcgccgc agcctccgca 60

gtccgcacct gcctccacga cctgtcgtgc tcgtgcgcta ctctcctcga gcgcggcgcg 120

gagcacgggg acatcaa atg gcg gca gcg gcg gag atc ggt ggt ttc gcg 170

Met Ala Ala Ala Ala Glu Ile Gly Gly Phe Ala
1 5 10

gcg gcg aga gtg gcg gtg gca acg ctc agg ccg gct gcg cac cca gcc 218

Ala Ala Arg Val Ala Val Ala Thr Leu Arg Pro Ala Ala His Pro Ala
15 20 25

ccg gcg gcg gcg gcg gca ccg cag cct agg agg gcg gtg gcg gcg cag 266

Pro Ala Ala Ala Ala Ala Pro Gln Pro Arg Arg Ala Val Ala Ala Gln
30 35 40

tcg ctg cag acg acc gcc acc gag gcg ctg acg gcg gat ctc gcc ggc 314

Ser Leu Gln Thr Thr Ala Thr Glu Ala Leu Thr Ala Asp Leu Ala Gly

45	50	55	
acg acc aac ggc gct gtg cat gct cgg atg aat agt aag gct aca agt			362
Thr Thr Asn Gly Ala Val His Ala Arg Met Asn Ser Lys Ala Thr Ser			
60	65	70	75
gaa atc act tca cag gca gtt act gca aat tct agg aga aag aca aag			410
Glu Ile Thr Ser Gln Ala Val Thr Ala Asn Ser Arg Arg Lys Thr Lys			
	80	85	90
ata gtc tgc acc ata ggt ccc tca acc aac act cgt gag atg att tgg			458
Ile Val Cys Thr Ile Gly Pro Ser Thr Asn Thr Arg Glu Met Ile Trp			
	95	100	105
aag ctt gca gag act gga atg aat gta gcg cgc ctt aat atg tcc cat			506
Lys Leu Ala Glu Thr Gly Met Asn Val Ala Arg Leu Asn Met Ser His			
	110	115	120
ggt gac cac cag tcg cac cag aag gtt att gat ttg gtc aag gag tac			554
Gly Asp His Gln Ser His Gln Lys Val Ile Asp Leu Val Lys Glu Tyr			
	125	130	135
aat gca cag aac act gat ggc aat gtt att gcc att atg ctg gac aca			602
Asn Ala Gln Asn Thr Asp Gly Asn Val Ile Ala Ile Met Leu Asp Thr			
	140	145	155
aag ggt cct gaa gtt aga agt ggg gat gtt cca gag cca atc atg ctc			650
Lys Gly Pro Glu Val Arg Ser Gly Asp Val Pro Glu Pro Ile Met Leu			
	160	165	170
aag gaa ggt caa gag ttc aac ttc acg att aaa aga ggg gtg agc act			698
Lys Glu Gly Gln Glu Phe Asn Phe Thr Ile Lys Arg Gly Val Ser Thr			
	175	180	185
gaa gac act gtc agc gtg aac tat gat gac ttc ata aat gat gtt gaa			746
Glu Asp Thr Val Ser Val Asn Tyr Asp Asp Phe Ile Asn Asp Val Glu			
	190	195	200
gct ggc gac ata cta tta gtg gat gga gga atg atg tcg ctt gct gtg			794
Ala Gly Asp Ile Leu Leu Val Asp Gly Gly Met Met Ser Leu Ala Val			
	205	210	215
aag tct aaa aca gcc gat aca gtc aag tgt aaa gta gtt gat ggt ggg			842
Lys Ser Lys Thr Ala Asp Thr Val Lys Cys Lys Val Val Asp Gly Gly			
	220	225	235
gaa ttg aaa tca cgg cgc cac cta aat gtc cgt gga aag agt gct act			890
Glu Leu Lys Ser Arg Arg His Leu Asn Val Arg Gly Lys Ser Ala Thr			

240	245	250	
ttg cca tct atc act gag aag gat tgg gaa gac ata aaa ttt ggt gtc			938
Leu Pro Ser Ile Thr Glu Lys Asp Trp Glu Asp Ile Lys Phe Gly Val			
255	260	265	
gaa aac ggt gtt gat ttc tat gca gtt tcc ttt gtg aag gat gcc aaa			986
Glu Asn Gly Val Asp Phe Tyr Ala Val Ser Phe Val Lys Asp Ala Lys			
270	275	280	
gtt atc cat gaa tta aaa gac tac ctt aaa agt gct aat gcc gat ata			1034
Val Ile His Glu Leu Lys Asp Tyr Leu Lys Ser Ala Asn Ala Asp Ile			
285	290	295	
cat gtc att cca aaa att gaa agt gca gat tca ata cca aac ctg cag			1082
His Val Ile Pro Lys Ile Glu Ser Ala Asp Ser Ile Pro Asn Leu Gln			
300	305	310	315
tcc att att gct gct tca gat ggg gca atg gtg gcg cgt gga gac ctt			1130
Ser Ile Ile Ala Ala Ser Asp Gly Ala Met Val Ala Arg Gly Asp Leu			
320	325	330	
ggt gct gaa ctt ccg att gag gat gtt cct ttg cta cag gca gag att			1178
Gly Ala Glu Leu Pro Ile Glu Asp Val Pro Leu Leu Gln Ala Glu Ile			
335	340	345	
gtc caa aca tgt cga agc atg gag aaa cca gtc att gtc gct aca aat			1226
Val Gln Thr Cys Arg Ser Met Glu Lys Pro Val Ile Val Ala Thr Asn			
350	355	360	
atg ttg gaa agc atg att gac cat cct act ccc act agg gca gaa gtt			1274
Met Leu Glu Ser Met Ile Asp His Pro Thr Pro Thr Arg Ala Glu Val			
365	370	375	
tct gac ata gct att gca gtt cgg gaa ggt gct gat gcc atc atg tta			1322
Ser Asp Ile Ala Ile Ala Val Arg Glu Gly Ala Asp Ala Ile Met Leu			
380	385	390	395
tct ggc gaa act gct cat gga aag tat cca cta aag gca gtc aag gtg			1370
Ser Gly Glu Thr Ala His Gly Lys Tyr Pro Leu Lys Ala Val Lys Val			
400	405	410	
atg cac act gtg gca ctc aga aca gaa tcc agc ctt tat aac cca act			1418
Met His Thr Val Ala Leu Arg Thr Glu Ser Ser Leu Tyr Asn Pro Thr			
415	420	425	
act tct cct agt ctt gtt gca tct gca cag ggt cta cag aat gag gac			1466
Thr Ser Pro Ser Leu Val Ala Ser Ala Gln Gly Leu Gln Asn Glu Asp			

430

435

440

ttc tcc gca agc cag cta agt aaa atg ttc gga tct cat gca acg atg 1514
 Phe Ser Ala Ser Gln Leu Ser Lys Met Phe Gly Ser His Ala Thr Met
 445 450 455

atg gcc aac acc ctt cgc aca cca atc att gta ttt aca cag aca ggc 1562
 Met Ala Asn Thr Leu Arg Thr Pro Ile Ile Val Phe Thr Gln Thr Gly
 460 465 470 475

tcc atg gct gtc ctc ctg agc cac tat cgt ccc tcg tct aca cta ttt 1610
 Ser Met Ala Val Leu Leu Ser His Tyr Arg Pro Ser Ser Thr Leu Phe
 480 485 490

gca ttt aca aac gag gaa cga gtg aag caa cgg cta gca ctc tac cag 1658
 Ala Phe Thr Asn Glu Glu Arg Val Lys Gln Arg Leu Ala Leu Tyr Gln
 495 500 505

ggc gtc atc cct att cac atg cag ttc tct gac gac gca gaa gaa act 1706
 Gly Val Ile Pro Ile His Met Gln Phe Ser Asp Asp Ala Glu Glu Thr
 510 515 520

ttc tcc aga gca att agc agc ttg ctg aaa gca caa tat gtg aag aag 1754
 Phe Ser Arg Ala Ile Ser Ser Leu Leu Lys Ala Gln Tyr Val Lys Lys
 525 530 535

gga gac tac gtc act ctt gtt cag agc gga gtg act tca atc tgg aga 1802
 Gly Asp Tyr Val Thr Leu Val Gln Ser Gly Val Thr Ser Ile Trp Arg
 540 545 550 555

gag gaa tcc act cac cac atc caa gtg agg aaa gtt cag gtc 1844
 Glu Glu Ser Thr His His Ile Gln Val Arg Lys Val Gln Val
 560 565

tgatgtgccg gtgggaattg gtcgtctgag aaattttgat agcgccgcct gatgtgttat 1904

catcattata tgtgtaattt tactgtttta ccaggagatt gctacgtcga gttatatgtt 1964

gtgtcgaatt cacgtgtagg ctctgaatct tgactgtgtt cgttcatttt cgcttgtttc 2024

acactgaagt gttataagct caactttact gcttttgttt tcttgtgaaa cttgagttta 2084

gtttcttggtt acaaaaggag ctagcactaa caggggtggtg agttttgtaa acggggcgag 2144

gactgttgag ttaaaactgt tgtaataatg atatcgttcc tgcaagacga cacatgcatg 2204

gccagaaggc caaagtcaaa aaaaaaaaaa aaaaaaaaaa a 2245

<210> 2

<211> 569

<212> PRT

<213> Zea mays

<400> 2

Met Ala Ala Ala Ala Glu Ile Gly Gly Phe Ala Ala Ala Arg Val Ala
1 5 10 15

Val Ala Thr Leu Arg Pro Ala Ala His Pro Ala Pro Ala Ala Ala Ala
20 25 30

Ala Pro Gln Pro Arg Arg Ala Val Ala Ala Gln Ser Leu Gln Thr Thr
35 40 45

Ala Thr Glu Ala Leu Thr Ala Asp Leu Ala Gly Thr Thr Asn Gly Ala
50 55 60

Val His Ala Arg Met Asn Ser Lys Ala Thr Ser Glu Ile Thr Ser Gln
65 70 75 80

Ala Val Thr Ala Asn Ser Arg Arg Lys Thr Lys Ile Val Cys Thr Ile
85 90 95

Gly Pro Ser Thr Asn Thr Arg Glu Met Ile Trp Lys Leu Ala Glu Thr
100 105 110

Gly Met Asn Val Ala Arg Leu Asn Met Ser His Gly Asp His Gln Ser
115 120 125

His Gln Lys Val Ile Asp Leu Val Lys Glu Tyr Asn Ala Gln Asn Thr
130 135 140

Asp Gly Asn Val Ile Ala Ile Met Leu Asp Thr Lys Gly Pro Glu Val
145 150 155 160

Arg Ser Gly Asp Val Pro Glu Pro Ile Met Leu Lys Glu Gly Gln Glu
165 170 175

Phe Asn Phe Thr Ile Lys Arg Gly Val Ser Thr Glu Asp Thr Val Ser
180 185 190

Val Asn Tyr Asp Asp Phe Ile Asn Asp Val Glu Ala Gly Asp Ile Leu
195 200 205

Leu Val Asp Gly Gly Met Met Ser Leu Ala Val Lys Ser Lys Thr Ala
210 215 220

Asp	Thr	Val	Lys	Cys	Lys	Val	Val	Asp	Gly	Gly	Glu	Leu	Lys	Ser	Arg	225	230	235	240
Arg	His	Leu	Asn	Val	Arg	Gly	Lys	Ser	Ala	Thr	Leu	Pro	Ser	Ile	Thr	245	250	255	
Glu	Lys	Asp	Trp	Glu	Asp	Ile	Lys	Phe	Gly	Val	Glu	Asn	Gly	Val	Asp	260	265	270	
Phe	Tyr	Ala	Val	Ser	Phe	Val	Lys	Asp	Ala	Lys	Val	Ile	His	Glu	Leu	275	280	285	
Lys	Asp	Tyr	Leu	Lys	Ser	Ala	Asn	Ala	Asp	Ile	His	Val	Ile	Pro	Lys	290	295	300	
Ile	Glu	Ser	Ala	Asp	Ser	Ile	Pro	Asn	Leu	Gln	Ser	Ile	Ile	Ala	Ala	305	310	315	320
Ser	Asp	Gly	Ala	Met	Val	Ala	Arg	Gly	Asp	Leu	Gly	Ala	Glu	Leu	Pro	325	330	335	
Ile	Glu	Asp	Val	Pro	Leu	Leu	Gln	Ala	Glu	Ile	Val	Gln	Thr	Cys	Arg	340	345	350	
Ser	Met	Glu	Lys	Pro	Val	Ile	Val	Ala	Thr	Asn	Met	Leu	Glu	Ser	Met	355	360	365	
Ile	Asp	His	Pro	Thr	Pro	Thr	Arg	Ala	Glu	Val	Ser	Asp	Ile	Ala	Ile	370	375	380	
Ala	Val	Arg	Glu	Gly	Ala	Asp	Ala	Ile	Met	Leu	Ser	Gly	Glu	Thr	Ala	385	390	395	400
His	Gly	Lys	Tyr	Pro	Leu	Lys	Ala	Val	Lys	Val	Met	His	Thr	Val	Ala	405	410	415	
Leu	Arg	Thr	Glu	Ser	Ser	Leu	Tyr	Asn	Pro	Thr	Thr	Ser	Pro	Ser	Leu	420	425	430	
Val	Ala	Ser	Ala	Gln	Gly	Leu	Gln	Asn	Glu	Asp	Phe	Ser	Ala	Ser	Gln	435	440	445	
Leu	Ser	Lys	Met	Phe	Gly	Ser	His	Ala	Thr	Met	Met	Ala	Asn	Thr	Leu	450	455	460	
Arg	Thr	Pro	Ile	Ile	Val	Phe	Thr	Gln	Thr	Gly	Ser	Met	Ala	Val	Leu	465	470	475	480

Leu Ser His Tyr Arg Pro Ser Ser Thr Leu Phe Ala Phe Thr Asn Glu
 485 490 495

Glu Arg Val Lys Gln Arg Leu Ala Leu Tyr Gln Gly Val Ile Pro Ile
 500 505 510

His Met Gln Phe Ser Asp Asp Ala Glu Glu Thr Phe Ser Arg Ala Ile
 515 520 525

Ser Ser Leu Leu Lys Ala Gln Tyr Val Lys Lys Gly Asp Tyr Val Thr
 530 535 540

Leu Val Gln Ser Gly Val Thr Ser Ile Trp Arg Glu Glu Ser Thr His
 545 550 555 560

His Ile Gln Val Arg Lys Val Gln Val
 565

<210> 3
 <211> 1922
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (148)..(1674)

<400> 3
 cccggggaag aatccttctc gacgccgccc ccattcattc ttggagggca agaagaacgc 60
 gcagtccaaa agcgaaacaa ggggaagggg cgaggcagcc aaacgaatcc cagcacctgc 120
 ctctcctttg cttgcgcaga tctagcg atg gcg gcg ggc ggt gag ttg gcg tgg 174
 Met Ala Ala Gly Gly Glu Leu Ala Trp
 1 5

ggg gag gag ccc gtg gcg cgg cgc cgg cct aag acc aag atc gtc tgc 222
 Gly Glu Glu Pro Val Ala Arg Arg Arg Pro Lys Thr Lys Ile Val Cys
 10 15 20 25

acg ctc ggc ccg gcg tcg cga tcc gtc gag atg atc tcg cgc ctg ctg 270
 Thr Leu Gly Pro Ala Ser Arg Ser Val Glu Met Ile Ser Arg Leu Leu
 30 35 40

cgc gcc ggg atg tgc gtc gcg cgc ttc aac ttc tcc cat ggc tcc cac 318

Arg	Ala	Gly	Met	Cys	Val	Ala	Arg	Phe	Asn	Phe	Ser	His	Gly	Ser	His		
			45						50					55			
gag tac cac cag gag acg ctc gac aac ctg cac gcc gcc atg gag ctc 366																	
Glu	Tyr	His	Gln	Glu	Thr	Leu	Asp	Asn	Leu	His	Ala	Ala	Met	Glu	Leu		
		60					65					70					
acc ggg atc ctc tgc gcc gtt atg ctc gac acc aag ggt cca gag att 414																	
Thr	Gly	Ile	Leu	Cys	Ala	Val	Met	Leu	Asp	Thr	Lys	Gly	Pro	Glu	Ile		
	75					80					85						
aga act gga ttt ttg aaa gat ggg aag cct att caa ttg ata aaa ggc 462																	
Arg	Thr	Gly	Phe	Leu	Lys	Asp	Gly	Lys	Pro	Ile	Gln	Leu	Ile	Lys	Gly		
	90				95				100					105			
caa gaa atc aca att tct aca gac tat agc att cag ggt gat gag aaa 510																	
Gln	Glu	Ile	Thr	Ile	Ser	Thr	Asp	Tyr	Ser	Ile	Gln	Gly	Asp	Glu	Lys		
			110				115					120					
atg ata tca atg agc tac aag aag ctt gct gtt gat ctg aag cca ggc 558																	
Met	Ile	Ser	Met	Ser	Tyr	Lys	Lys	Leu	Ala	Val	Asp	Leu	Lys	Pro	Gly		
			125				130					135					
agt gtc ata ttg tgt gct gat ggt acc atc act ctt act gtt ctt cac 606																	
Ser	Val	Ile	Leu	Cys	Ala	Asp	Gly	Thr	Ile	Thr	Leu	Thr	Val	Leu	His		
		140				145					150						
tgt gat aaa gaa caa ggc ttg gtt cgc tgc cgc tgt gag aac act ttc 654																	
Cys	Asp	Lys	Glu	Gln	Gly	Leu	Val	Arg	Cys	Arg	Cys	Glu	Asn	Thr	Phe		
	155					160				165							
aag ctt ggc gag agg aag aat gtt aat ctt cca gga gtt att gtt gat 702																	
Lys	Leu	Gly	Glu	Arg	Lys	Asn	Val	Asn	Leu	Pro	Gly	Val	Ile	Val	Asp		
	170				175				180				185				
ctc ccc aca ctc aca gac aag gac aag gag gac atc ctt aaa tgg ggt 750																	
Leu	Pro	Thr	Leu	Thr	Asp	Lys	Asp	Lys	Glu	Asp	Ile	Leu	Lys	Trp	Gly		
			190				195					200					
gtt cca aac aag att gac atg att gcc ttg tca ttt gtt cgg aag ggt 798																	
Val	Pro	Asn	Lys	Ile	Asp	Met	Ile	Ala	Leu	Ser	Phe	Val	Arg	Lys	Gly		
			205				210					215					
tcg gat ctt gtg gag gtt agg aag gta ctt ggt gag cat gcc aag tcc 846																	
Ser	Asp	Leu	Val	Glu	Val	Arg	Lys	Val	Leu	Gly	Glu	His	Ala	Lys	Ser		
		220				225					230						
ata atg ctg atg tca aag gtt gag aat caa gag gga gta gct aac ttt 894																	

Ile Met Leu Met Ser Lys Val Glu Asn Gln Glu Gly Val Ala Asn Phe
 235 240 245

gat gat atc ctg gca aac tct gat gct ttt atg gtg gca aga ggt gat 942
 Asp Asp Ile Leu Ala Asn Ser Asp Ala Phe Met Val Ala Arg Gly Asp
 250 255 260 265

tta gga atg gaa att cct ata gag aag att ttc ttt gca cag aag gtg 990
 Leu Gly Met Glu Ile Pro Ile Glu Lys Ile Phe Phe Ala Gln Lys Val
 270 275 280

atg att ttc aag tgc aat att caa ggc aag cct gtt gtg act gca acc 1038
 Met Ile Phe Lys Cys Asn Ile Gln Gly Lys Pro Val Val Thr Ala Thr
 285 290 295

cag atg ttg gaa tct atg atc aag tct cct cgc cct act cgg gca gaa 1086
 Gln Met Leu Glu Ser Met Ile Lys Ser Pro Arg Pro Thr Arg Ala Glu
 300 305 310

gca acg gat gtt gca aac gca gtt ctt gat ggc aca gac tgt gtt atg 1134
 Ala Thr Asp Val Ala Asn Ala Val Leu Asp Gly Thr Asp Cys Val Met
 315 320 325

ctc agt ggt gag act gct gct ggg gct tat cca ggg ttg gcg gtg cag 1182
 Leu Ser Gly Glu Thr Ala Ala Gly Ala Tyr Pro Gly Leu Ala Val Gln
 330 335 340 345

act atg gct aag atc tgc ctg caa gca gag tct tgc gta gac cat gct 1230
 Thr Met Ala Lys Ile Cys Leu Gln Ala Glu Ser Cys Val Asp His Ala
 350 355 360

gct att ttc aaa tca atc atg gct tca gct cca att cca atg agt cca 1278
 Ala Ile Phe Lys Ser Ile Met Ala Ser Ala Pro Ile Pro Met Ser Pro
 365 370 375

ttg gag agc ctt gca tca tca gct gtt cgc aca gca aac tct gcc agg 1326
 Leu Glu Ser Leu Ala Ser Ser Ala Val Arg Thr Ala Asn Ser Ala Arg
 380 385 390

gca gca ctt atc ttg gtc ctg acc agg gga gga act act gct agg ctt 1374
 Ala Ala Leu Ile Leu Val Leu Thr Arg Gly Gly Thr Thr Ala Arg Leu
 395 400 405

gta gcc aag tat agg cca tcc atg ccg att ctg tcc gtt gtg gtt cct 1422
 Val Ala Lys Tyr Arg Pro Ser Met Pro Ile Leu Ser Val Val Val Pro
 410 415 420 425

gag ctg aag aca gac tcg ttc gac tgg gcc tgc agt gac gag ggt ccg 1470

Glu Leu Lys Thr Asp Ser Phe Asp Trp Ala Cys Ser Asp Glu Gly Pro
 430 435 440

gca agg cac agc ctc att gtg agg ggt gtc atc cca atg ctg agt gcc 1518
 Ala Arg His Ser Leu Ile Val Arg Gly Val Ile Pro Met Leu Ser Ala
 445 450 455

gcc act gcc aag gcc ttt gac aac gaa gcc act gac gaa gct att ggt 1566
 Ala Thr Ala Lys Ala Phe Asp Asn Glu Ala Thr Asp Glu Ala Ile Gly
 460 465 470

ttt gcc att gaa aat gcg aag acg atg ggg cta tgc aac acc ggt caa 1614
 Phe Ala Ile Glu Asn Ala Lys Thr Met Gly Leu Cys Asn Thr Gly Gln
 475 480 485

tcc gtt gtg gcc ctg cac cgc atc ggg att tca tcc gtc atc aag ctt 1662
 Ser Val Val Ala Leu His Arg Ile Gly Ile Ser Ser Val Ile Lys Leu
 490 495 500 505

ctt act gtg aag taggggtcca aggggtgagg acaccatttt gcttggtgaa 1714
 Leu Thr Val Lys

tttttgtgag gctgcttacg cacatcagcg tatccacagc ttttctgttg ccaaagatac 1774

agactttgcg ttctggtaca ccttggtggtt acaagggtgtt gggaatttgt cgtttagata 1834

ttagcgattt aaacagttta tcaactgota tagctaatta atttgcagct gtgctgcaac 1894

tttatcgtac tgaaaaaaaa aaaaaaaaa 1922

<210> 4
 <211> 509
 <212> PRT
 <213> Zea mays

<400> 4
 Met Ala Ala Gly Gly Glu Leu Ala Trp Gly Glu Glu Pro Val Ala Arg
 1 5 10 15

Arg Arg Pro Lys Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Ser Arg
 20 25 30

Ser Val Glu Met Ile Ser Arg Leu Leu Arg Ala Gly Met Cys Val Ala
 35 40 45

Arg Phe Asn Phe Ser His Gly Ser His Glu Tyr His Gln Glu Thr Leu
 50 55 60

Asp Asn Leu His Ala Ala Met Glu Leu Thr Gly Ile Leu Cys Ala Val
65 70 75 80

Met Leu Asp Thr Lys Gly Pro Glu Ile Arg Thr Gly Phe Leu Lys Asp
85 90 95

Gly Lys Pro Ile Gln Leu Ile Lys Gly Gln Glu Ile Thr Ile Ser Thr
100 105 110

Asp Tyr Ser Ile Gln Gly Asp Glu Lys Met Ile Ser Met Ser Tyr Lys
115 120 125

Lys Leu Ala Val Asp Leu Lys Pro Gly Ser Val Ile Leu Cys Ala Asp
130 135 140

Gly Thr Ile Thr Leu Thr Val Leu His Cys Asp Lys Glu Gln Gly Leu
145 150 155 160

Val Arg Cys Arg Cys Glu Asn Thr Phe Lys Leu Gly Glu Arg Lys Asn
165 170 175

Val Asn Leu Pro Gly Val Ile Val Asp Leu Pro Thr Leu Thr Asp Lys
180 185 190

Asp Lys Glu Asp Ile Leu Lys Trp Gly Val Pro Asn Lys Ile Asp Met
195 200 205

Ile Ala Leu Ser Phe Val Arg Lys Gly Ser Asp Leu Val Glu Val Arg
210 215 220

Lys Val Leu Gly Glu His Ala Lys Ser Ile Met Leu Met Ser Lys Val
225 230 235 240

Glu Asn Gln Glu Gly Val Ala Asn Phe Asp Asp Ile Leu Ala Asn Ser
245 250 255

Asp Ala Phe Met Val Ala Arg Gly Asp Leu Gly Met Glu Ile Pro Ile
260 265 270

Glu Lys Ile Phe Phe Ala Gln Lys Val Met Ile Phe Lys Cys Asn Ile
275 280 285

Gln Gly Lys Pro Val Val Thr Ala Thr Gln Met Leu Glu Ser Met Ile
290 295 300

Lys Ser Pro Arg Pro Thr Arg Ala Glu Ala Thr Asp Val Ala Asn Ala
305 310 315 320

Val Leu Asp Gly Thr Asp Cys Val Met Leu Ser Gly Glu Thr Ala Ala
 325 330 335

Gly Ala Tyr Pro Gly Leu Ala Val Gln Thr Met Ala Lys Ile Cys Leu
 340 345 350

Gln Ala Glu Ser Cys Val Asp His Ala Ala Ile Phe Lys Ser Ile Met
 355 360 365

Ala Ser Ala Pro Ile Pro Met Ser Pro Leu Glu Ser Leu Ala Ser Ser
 370 375 380

Ala Val Arg Thr Ala Asn Ser Ala Arg Ala Ala Leu Ile Leu Val Leu
 385 390 395 400

Thr Arg Gly Gly Thr Thr Ala Arg Leu Val Ala Lys Tyr Arg Pro Ser
 405 410 415

Met Pro Ile Leu Ser Val Val Val Pro Glu Leu Lys Thr Asp Ser Phe
 420 425 430

Asp Trp Ala Cys Ser Asp Glu Gly Pro Ala Arg His Ser Leu Ile Val
 435 440 445

Arg Gly Val Ile Pro Met Leu Ser Ala Ala Thr Ala Lys Ala Phe Asp
 450 455 460

Asn Glu Ala Thr Asp Glu Ala Ile Gly Phe Ala Ile Glu Asn Ala Lys
 465 470 475 480

Thr Met Gly Leu Cys Asn Thr Gly Gln Ser Val Val Ala Leu His Arg
 485 490 495

Ile Gly Ile Ser Ser Val Ile Lys Leu Leu Thr Val Lys
 500 505

<210> 5
 <211> 2075
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (198)..(1736)

<400> 5

gcgcccacgg aatcgcaatt cccactccc accccccttc tcctttctat aaagggaac 60

ttcgccacca aatctogaat cccatctcgc tgctctccgc cgctcgacgc cgacgccgac 120

gccgacacct ctccctcccc cattccccgt gccccggacc gcggagcaga cagaggcgag 180

atccggagcg ccgcgcg atg gcg aac atc gac atg gcg aag atc ctg gcg 230
Met Ala Asn Ile Asp Met Ala Lys Ile Leu Ala
1 5 10

gac ctg gac cgc ggc gcc ggc gac gcg cgg ctg ccc aag acc aag ctc 278
Asp Leu Asp Arg Gly Ala Gly Asp Ala Arg Leu Pro Lys Thr Lys Leu
15 20 25

gtc tgc acg ctt ggc ccg gcc tcc cgc tcc gtg ccc atg ctc gag aag 326
Val Cys Thr Leu Gly Pro Ala Ser Arg Ser Val Pro Met Leu Glu Lys
30 35 40

ctg ctc cgc gcc ggc atg aac gtc gcg cgc ttc aac ttc tcc cac ggc 374
Leu Leu Arg Ala Gly Met Asn Val Ala Arg Phe Asn Phe Ser His Gly
45 50 55

acc cac cag tac cac cag gag acg ctc gac agc ctc cgc cag gcc atg 422
Thr His Gln Tyr His Gln Glu Thr Leu Asp Ser Leu Arg Gln Ala Met
60 65 70 75

cac aac acc ggc atc ctc tgc gcc gtc atg ctc gac acc aag ggt cct 470
His Asn Thr Gly Ile Leu Cys Ala Val Met Leu Asp Thr Lys Gly Pro
80 85 90

gag att cgt aca ggg ttt ttg aag gat ggt aaa cca att aag cta acc 518
Glu Ile Arg Thr Gly Phe Leu Lys Asp Gly Lys Pro Ile Lys Leu Thr
95 100 105

aag ggt caa gag atc act gtt acc act gat tat gat atc aag ggt gac 566
Lys Gly Gln Glu Ile Thr Val Thr Thr Asp Tyr Asp Ile Lys Gly Asp
110 115 120

gaa aaa atg atc gct atg agt tac aag aaa ctg cct gtt gac gtg aag 614
Glu Lys Met Ile Ala Met Ser Tyr Lys Lys Leu Pro Val Asp Val Lys
125 130 135

cct gga aat gtc ata ctc tgc gca gat ggt act atc tct ctg gcc gtt 662
Pro Gly Asn Val Ile Leu Cys Ala Asp Gly Thr Ile Ser Leu Ala Val
140 145 150 155

ctg tct tgc gat cct gat gct gga act gtg cgt tgt agg tgt gag aac 710

Leu Ser Cys Asp Pro Asp Ala Gly Thr Val Arg Cys Arg Cys Glu Asn	
160 165 170	
act gca atg ctt ggt gag aga aag aac tgc aat ttg cca gga att gtt	758
Thr Ala Met Leu Gly Glu Arg Lys Asn Cys Asn Leu Pro Gly Ile Val	
175 180 185	
gtg gat ctt cct aca ttg act gag aaa gat aaa gaa gat att ttg ggc	806
Val Asp Leu Pro Thr Leu Thr Glu Lys Asp Lys Glu Asp Ile Leu Gly	
190 195 200	
tgg ggt gtt cca aat gac att gac atg att gct cta tcc ttt gtc cgt	854
Trp Gly Val Pro Asn Asp Ile Asp Met Ile Ala Leu Ser Phe Val Arg	
205 210 215	
aaa gga tca gat ttg gtg act gtc aga cag gtt ctt ggg cag cat gcc	902
Lys Gly Ser Asp Leu Val Thr Val Arg Gln Val Leu Gly Gln His Ala	
220 225 230 235	
aag cgc att aag ttg atg tca aag gtt gag aac caa gag ggt gtt gta	950
Lys Arg Ile Lys Leu Met Ser Lys Val Glu Asn Gln Glu Gly Val Val	
240 245 250	
aac ttt gat gag atc ttg agg gag act gat gct ttt atg gtt gct aga	998
Asn Phe Asp Glu Ile Leu Arg Glu Thr Asp Ala Phe Met Val Ala Arg	
255 260 265	
ggt gat ctg gga atg gag att cca gtc gag aag att ttc ctt gcg cag	1046
Gly Asp Leu Gly Met Glu Ile Pro Val Glu Lys Ile Phe Leu Ala Gln	
270 275 280	
aag atg atg atc tac aag tgc aac att gct ggc aaa cct gtt gtt act	1094
Lys Met Met Ile Tyr Lys Cys Asn Ile Ala Gly Lys Pro Val Val Thr	
285 290 295	
gct acc cag atg ctc gag tcg atg atc aaa tct cct cgg ccg aca cgt	1142
Ala Thr Gln Met Leu Glu Ser Met Ile Lys Ser Pro Arg Pro Thr Arg	
300 305 310 315	
gct gag gcc act gac gtt gca aat gcc gtt ctt gat gga act gac tgt	1190
Ala Glu Ala Thr Asp Val Ala Asn Ala Val Leu Asp Gly Thr Asp Cys	
320 325 330	
gtc atg ctc agc gga gag agt gcc gct gga gcc tac ccc gag gtg gct	1238
Val Met Leu Ser Gly Glu Ser Ala Ala Gly Ala Tyr Pro Glu Val Ala	
335 340 345	
gtg aag atc atg gct cgt att tgc atc gag gca gaa tct tcc ctg gac	1286

Val Lys Ile Met Ala Arg Ile Cys Ile Glu Ala Glu Ser Ser Leu Asp
 350 355 360

cac gag gca gtt ttc aag gcc atg atc agg tcc gcg cct ctt cca atg 1334
 His Glu Ala Val Phe Lys Ala Met Ile Arg Ser Ala Pro Leu Pro Met
 365 370 375

agc cct ctg gag tcc ctt gca tca tct gct gtg agg act gcc aac aag 1382
 Ser Pro Leu Glu Ser Leu Ala Ser Ser Ala Val Arg Thr Ala Asn Lys
 380 385 390 395

gcc aag gct gca ctg att gtc gtc ctg act cgc ggt ggc acc acg gcc 1430
 Ala Lys Ala Ala Leu Ile Val Val Leu Thr Arg Gly Gly Thr Thr Ala
 400 405 410

aaa ctg gtc gcc aag tac cgc ccc agg gtc ccc atc ctc tcc gtt gtc 1478
 Lys Leu Val Ala Lys Tyr Arg Pro Arg Val Pro Ile Leu Ser Val Val
 415 420 425

gta ccc gtg ctt acg acc gac tct ttc gac tgg acc atc agc tcc gag 1526
 Val Pro Val Leu Thr Thr Asp Ser Phe Asp Trp Thr Ile Ser Ser Glu
 430 435 440

ggc cca gct agg cac agc ctg atc tac aga ggc ctc att ccc ctc ctc 1574
 Gly Pro Ala Arg His Ser Leu Ile Tyr Arg Gly Leu Ile Pro Leu Leu
 445 450 455

gcc gag ggc tcc gcg aag gct acg gat tca gag tcg acg gag gtg atc 1622
 Ala Glu Gly Ser Ala Lys Ala Thr Asp Ser Glu Ser Thr Glu Val Ile
 460 465 470 475

ctt gag gcc gcg ttg aag tcg gcc gtg cag aag cag ctc tgc aag cct 1670
 Leu Glu Ala Ala Leu Lys Ser Ala Val Gln Lys Gln Leu Cys Lys Pro
 480 485 490

ggt gat gcc atc gtg gct ctt cat cgt att ggc gtc gcc tcc gtc atc 1718
 Gly Asp Ala Ile Val Ala Leu His Arg Ile Gly Val Ala Ser Val Ile
 495 500 505

aag atc tgc atc gtg aag tgatcaccac gacctggttc tcactgctgg 1766
 Lys Ile Cys Ile Val Lys
 510

gattccatga aacagctttt ctgcctcctt tttactgcat ttttttccgg agacagatat 1826

ttatgttgta agcctgcgtc tgttggttgc agttgcggaa tgttttttgt tcacgtagtt 1886

atttagctgg taaatgggga gggagaggac tccattgatg ttagtggttaa taagatttgt 1946

gtctatggag ttgagttgaa agggtttttt catgctaagc cccgagacac taggagatgg 2006

agatcgaggt tgagatgaga taagcaataa gtgaaaaaaaa tgttgatttg caaaaaaaaa 2066

aaaaaaaaa 2075

<210> 6

<211> 513

<212> PRT

<213> Zea mays

<400> 6

Met Ala Asn Ile Asp Met Ala Lys Ile Leu Ala Asp Leu Asp Arg Gly
1 5 10 15

Ala Gly Asp Ala Arg Leu Pro Lys Thr Lys Leu Val Cys Thr Leu Gly
20 25 30

Pro Ala Ser Arg Ser Val Pro Met Leu Glu Lys Leu Leu Arg Ala Gly
35 40 45

Met Asn Val Ala Arg Phe Asn Phe Ser His Gly Thr His Gln Tyr His
50 55 60

Gln Glu Thr Leu Asp Ser Leu Arg Gln Ala Met His Asn Thr Gly Ile
65 70 75 80

Leu Cys Ala Val Met Leu Asp Thr Lys Gly Pro Glu Ile Arg Thr Gly
85 90 95

Phe Leu Lys Asp Gly Lys Pro Ile Lys Leu Thr Lys Gly Gln Glu Ile
100 105 110

Thr Val Thr Thr Asp Tyr Asp Ile Lys Gly Asp Glu Lys Met Ile Ala
115 120 125

Met Ser Tyr Lys Lys Leu Pro Val Asp Val Lys Pro Gly Asn Val Ile
130 135 140

Leu Cys Ala Asp Gly Thr Ile Ser Leu Ala Val Leu Ser Cys Asp Pro
145 150 155 160

Asp Ala Gly Thr Val Arg Cys Arg Cys Glu Asn Thr Ala Met Leu Gly
165 170 175

Glu Arg Lys Asn Cys Asn Leu Pro Gly Ile Val Val Asp Leu Pro Thr

180	185	190
Leu Thr Glu Lys Asp Lys Glu Asp Ile Leu Gly Trp Gly Val Pro Asn		
195	200	205
Asp Ile Asp Met Ile Ala Leu Ser Phe Val Arg Lys Gly Ser Asp Leu		
210	215	220
Val Thr Val Arg Gln Val Leu Gly Gln His Ala Lys Arg Ile Lys Leu		
225	230	235 240
Met Ser Lys Val Glu Asn Gln Glu Gly Val Val Asn Phe Asp Glu Ile		
245	250	255
Leu Arg Glu Thr Asp Ala Phe Met Val Ala Arg Gly Asp Leu Gly Met		
260	265	270
Glu Ile Pro Val Glu Lys Ile Phe Leu Ala Gln Lys Met Met Ile Tyr		
275	280	285
Lys Cys Asn Ile Ala Gly Lys Pro Val Val Thr Ala Thr Gln Met Leu		
290	295	300
Glu Ser Met Ile Lys Ser Pro Arg Pro Thr Arg Ala Glu Ala Thr Asp		
305	310	315 320
Val Ala Asn Ala Val Leu Asp Gly Thr Asp Cys Val Met Leu Ser Gly		
325	330	335
Glu Ser Ala Ala Gly Ala Tyr Pro Glu Val Ala Val Lys Ile Met Ala		
340	345	350
Arg Ile Cys Ile Glu Ala Glu Ser Ser Leu Asp His Glu Ala Val Phe		
355	360	365
Lys Ala Met Ile Arg Ser Ala Pro Leu Pro Met Ser Pro Leu Glu Ser		
370	375	380
Leu Ala Ser Ser Ala Val Arg Thr Ala Asn Lys Ala Lys Ala Ala Leu		
385	390	395 400
Ile Val Val Leu Thr Arg Gly Gly Thr Thr Ala Lys Leu Val Ala Lys		
405	410	415
Tyr Arg Pro Arg Val Pro Ile Leu Ser Val Val Val Pro Val Leu Thr		
420	425	430
Thr Asp Ser Phe Asp Trp Thr Ile Ser Ser Glu Gly Pro Ala Arg His		

435	440	445
Ser Leu Ile Tyr Arg Gly Leu Ile Pro Leu Leu Ala Glu Gly Ser Ala		
450	455	460
Lys Ala Thr Asp Ser Glu Ser Thr Glu Val Ile Leu Glu Ala Ala Leu		
465	470	475
Lys Ser Ala Val Gln Lys Gln Leu Cys Lys Pro Gly Asp Ala Ile Val		
485	490	495
Ala Leu His Arg Ile Gly Val Ala Ser Val Ile Lys Ile Cys Ile Val		
500	505	510
Lys		